

#2

OIFE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/843,377
 DATE: 05/14/2001
 TIME: 09:23:55

Input Set : A:\RTS-0235 Sequence Listing.txt
 Output Set: N:\CRF3\05142001\I843377.raw

ENTERED

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6 <110> APPLICANT: C. Frank Bennett
7   Andrew T. Watt
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF INTERFERON GAMMA RECEPTOR 2 EXPRESSION
11 <130> FILE REFERENCE: RTS-0235
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/843,377
C--> 13 <141> CURRENT FILING DATE: 2001-04-26
13 <160> NUMBER OF SEQ ID NOS: 89
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctccctcaggg          20
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga          20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 2214
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
48 <221> NAME/KEY: CDS
49 <222> LOCATION: (649)...(1662)
51 <400> SEQUENCE: 3
52 gttgactgga ggcggagggtt gcagtgagcc gagatcgccc cactgcactc cagcctggtg          60
54 actccgtctc aaaaaaaagg ggaggggggc gggggagagt tgaagctta atatgtactt          120
56 tgggggctat taagcaaac attcgacta aaggggcgaa tctcgaaatt gtgcgatcaa          180
58 gcaccocaga ggagagttag ggagggtcag gaggggtggg ggctccaggg aacgcccggg          240
60 ggcttggggc ggggtctcgc ggggcccttc cggaaggatc gcggcccccg aaggtggggc          300
62 tcccgcgggg ctccagtcct caggacgttc cgggaggctc cgcgctctgg gagggccgct          360
64 gcgtggggtc ccgcgcgtgc agccgcagag gcccccagg gccgcggttc ccggagcggg          420
66 aaagtccgcg gcggggcggg tggctcggg ggccgggaagg ggccggggcg gggggcgggg          480
68 cggccgagcc gaatcccctc caccgggagc ccccgctgcc gctcgggaag agcgcgggccc          540
70 tgcgcgccct gcgctcgcca tggcggtttg ggcggcgagc tgagcggctc cgcggacccc          600
72 gagcgggggc ccggcccgca cctgagccgc cgcgagcgc ccgggggc atg cga cgg          657
73                                     1
74                                     Met Arg Pro
76 acg ctg ctg tgg tgg ctg ctg ctg ctg ctc gga gtc ttc gcc gcc gcc          705
77 Thr Leu Leu Trp Ser Leu Leu Leu Leu Gly Val Phe Ala Ala Ala
78       5              10              15

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80 gcc ggc gcc cgc cca gac cct ctt tcc cag ctg ccc gct cct cag cac      753
81 Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala Pro Gln His
82 20      25      30      35
84 cgc aag att cgc ctg tac aac gca gag cag gtc ctg agt tgg gag cca      801
85 Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser Trp Glu Pro
86 40      45      50
88 gtg gcc ctg agc aat agc acg agg cct gtt gtc tac cga gtg cag ttt      849
89 Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg Val Gln Phe
90 55      60      65
92 aaa tac acc gac agt aaa tgg ttc acg gcc gac atc atg tcc ata ggg      897
93 Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met Ser Ile Gly
94 70      75      80
96 gtg aat tgt aca cag atc aca gca aca gag tgt gac ttc act gcc gcc      945
97 Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe Thr Ala Ala
98 85      90      95
100 agt ccc tca gca ggc ttc cca atg gat ttc aat gtc act cta cgc ctt      993
101 Ser Pro Ser Ala Gly Phe Pro Met Asp Phe Asn Val Thr Leu Arg Leu
102 100      105      110      115
104 cga gct gag ctg gga gca ctc cat tct gcc tgg gtg aca atg cct tgg      1041
105 Arg Ala Glu Leu Gly Ala Leu His Ser Ala Trp Val Thr Met Pro Trp
106 120      125      130
108 ttt caa cac tat cgg aat gtg act gtc ggg cct cca gaa aac att gag      1089
109 Phe Gln His Tyr Arg Asn Val Thr Val Gly Pro Pro Glu Asn Ile Glu
110 135      140      145
112 gtg acc cca gga gaa ggc tcc ctc atc atc agg ttc tcc tct ccc ttt      1137
113 Val Thr Pro Gly Glu Gly Ser Leu Ile Ile Arg Phe Ser Pro Phe
114 150      155      160
116 gac atc gct gat acc tcc acg gcc ttt ttt tgt tat tat gtc cat tac      1185
117 Asp Ile Ala Asp Thr Ser Thr Ala Phe Phe Cys Tyr Tyr Val His Tyr
118 165      170      175
120 tgg gaa aaa gga gga atc caa cag gtc aaa ggc cct ttc aga agc aac      1233
121 Trp Glu Lys Gly Gly Ile Gln Gln Val Lys Gly Pro Phe Arg Ser Asn
122 180      185      190      195
124 tcc att tca ttg gat aac tta aaa ccc tcc aga gtg tac tgt tta caa      1281
125 Ser Ile Ser Leu Asp Asn Leu Lys Pro Ser Arg Val Tyr Cys Leu Gln
126 200      205      210
128 gtc cag gca caa ctg ctt tgg aac aaa agt aac atc ttt aga gtc ggg      1329
129 Val Gln Ala Gln Leu Leu Trp Asn Lys Ser Asn Ile Phe Arg Val Gly
130 215      220      225
132 cat tta agc aac ata tct tgc tac gaa aca atg gca gat gcc tcc act      1377
133 His Leu Ser Asn Ile Ser Cys Tyr Glu Thr Met Ala Asp Ala Ser Thr
134 230      235      240
136 gac ctt cag caa gtc atc ctg atc tcc gtg gga aca ttt tgc ttg ctg      1425
137 Glu Leu Gln Gln Val Ile Leu Ile Ser Val Gly Thr Phe Ser Leu Leu
138 245      250      255
140 tgg gtg ctg gca gga gcc tgt ttc ttc ctg gtc ctg aaa tat aga ggc      1473
141 Ser Val Leu Ala Gly Ala Cys Phe Phe Leu Val Leu Lys Tyr Arg Gly
142 260      265      270      275
144 ctg att aaa tac tgg ttt cac act cca cca agc atc cca tta cag ata      1521

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145 Leu Ile Lys Tyr Trp Phe His Thr Pro Pro Ser Ile Pro Leu Gln Ile
146                280                285                290
148 gaa gag tat tta aaa gac cca act cag ccc atc tta gag gcc ttg gac   1569
149 Glu Glu Tyr Leu Lys Asp Pro Thr Gln Pro Ile Leu Glu Ala Leu Asp
150                295                300                305
152 aag gac agc tca cca aag gat gac gtc tgg gac tct gtg tcc att atc   1617
153 Lys Asp Ser Ser Pro Lys Asp Asp Val Trp Asp Ser Val Ser Ile Ile
154                310                315                320
156 tcg ttt ccg gaa aag gag caa gaa gat gtt ctc caa acg-ctt tga   1662
157 Ser Phe Pro Glu Lys Glu Gln Glu Asp Val Leu Gln Thr Leu
158                325                330                335
160 accaaagcat gggcctagcc cactggctcc ctggaagaga tcaagccatc ggagctgcta   1722
162 gagttctgtc tggactttcc agagaccagt attccctttt gctgcctcta aaaggcctgt   1782
164 cctcgcagac atgagagaca gcaggtctca tgggggtgac aagctttttt ttttttttct   1842
166 taaagaattt tcaaaatcaa attccagaat gattttacgg agatatccca ggaaaattaa   1902
168 ggcttctctt aaacactaaa aaggcatgta attgcttggt agcaaaatgg atatgacaca   1962
170 tctctgatac ttttttcatt attggtlggg ctgagcagtc agaagacctg gtcgtgctct   2022
172 tgactttggc aaatgagccg gagccctctg ggcaggtcac acaacctgtc ccagcgaggg   2082
174 acactgagtg gcccttcctg tacatccatg gtgtgctggc ttaaaatgta attaatcttg   2142
176 taaatatact cctagtaatt taagattttg tttttaaact ggaataaaaa gatgtgatag   2202
178 tgcattgttt tt                2214

181 <210> SEQ ID NO: 4
182 <211> LENGTH: 18
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
188 <223> OTHER INFORMATION: PCR Primer
190 <400> SEQUENCE: 4
191 cagcaggcctt cccaatgg                18
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 19
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
201 <223> OTHER INFORMATION: PCR Primer
203 <400> SEQUENCE: 5
204 ggaggcccca cagtcacat                19
207 <210> SEQ ID NO: 6
208 <211> LENGTH: 28
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
214 <223> OTHER INFORMATION: PCR Probe
216 <400> SEQUENCE: 6
217 tcaatgtcac tctacgcctt cgagctga                28
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 19
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence

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225 <220> FEATURE:
227 <223> OTHER INFORMATION: PCR Primer
229 <400> SEQUENCE: 7
230 gaaggtgaag gtcggagtc 19
233 <210> SEQ ID NO: 8
234 <211> LENGTH: 20
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
240 <223> OTHER INFORMATION: PCR Primer
242 <400> SEQUENCE: 8
243 gaagatggtg atgggatttc 20
246 <210> SEQ ID NO: 9
247 <211> LENGTH: 20
248 <212> TYPE: DNA
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Probe
255 <400> SEQUENCE: 9
256 caagcttccc gttctcagcc 20
259 <210> SEQ ID NO: 10
260 <211> LENGTH: 339
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
264 <220> FEATURE:
266 <400> SEQUENCE: 10
267 ttttagtoga aatgtttgct ttaatagccc ccaaagtaca tattaagctt tcaactctcc 60
269 cccgcgccccc tcoccttttt tttagagcgg agtcaccagg ctggagtgcg gtggggcgat 120
271 ctggctcacc tgcaacctcc gcctccagtc aacccattt tgaagaagggt ttaatgggga 180
273 aggagttaga aagggccccag tgaaggagga ggtggggctc tgggggtggg gggaatggcc 240
275 tccgagcagg gggagggaga gacagaaact tccagcattt cttaatggcg tggggtttgc 300
277 ctggagccgg gcggcggtgc acgagtagga agtccttta 339
279 <210> SEQ ID NO: 11
280 <211> LENGTH: 54000
281 <212> TYPE: DNA
282 <213> ORGANISM: Homo sapiens
284 <220> FEATURE:
285 <221> NAME/KEY: exon
286 <222> LOCATION: (514)...(1420)
287 <223> OTHER INFORMATION: Exon 1
289 <221> NAME/KEY: intron
290 <222> LOCATION: (1421)...(12692)
291 <223> OTHER INFORMATION: Intron 1
293 <221> NAME/KEY: exon
294 <222> LOCATION: (12693)...(12825)
295 <223> OTHER INFORMATION: Exon 2
297 <221> NAME/KEY: intron
298 <222> LOCATION: (12826)...(19284)
299 <223> OTHER INFORMATION: Intron 2

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301 <221> NAME/KEY: exon
302 <222> LOCATION: (19285)...(19490)
303 <223> OTHER INFORMATION: Exon 3
305 <221> NAME/KEY: intron
306 <222> LOCATION: (19491)...(24688)
307 <223> OTHER INFORMATION: Intron 3
309 <221> NAME/KEY: exon
310 <222> LOCATION: (24689)...(24837)
311 <223> OTHER INFORMATION: Exon 4
313 <221> NAME/KEY: intron
314 <222> LOCATION: (24838)...(29981)
315 <223> OTHER INFORMATION: Intron 4
317 <221> NAME/KEY: exon
318 <222> LOCATION: (29982)...(30141)
319 <223> OTHER INFORMATION: Exon 5
321 <221> NAME/KEY: intron
322 <222> LOCATION: (30142)...(30518)
323 <223> OTHER INFORMATION: Intron 5
325 <221> NAME/KEY: exon
326 <222> LOCATION: (30519)...(30676)
327 <223> OTHER INFORMATION: Exon 6
329 <221> NAME/KEY: intron
330 <222> LOCATION: (30677)...(34632)
331 <223> OTHER INFORMATION: Intron 6
333 <221> NAME/KEY: exon
334 <222> LOCATION: (34633)...(35318)
335 <223> OTHER INFORMATION: Exon 7
337 <400> SEQUENCE: 11
338 ggctgggtctc caactcctgg cctcatgtga tcgccacc tcggcctcct aaagtgtga 60
339 gattacaggc gtgagccacc gcgcctggca tcagtgcata ctttttgaag tgattccaag 120
340 ttatgcgccg ctttttctgt gtaacatata aatacatctc tgtatctaga aataccaat 180
341 gcataattca attgtctgcg aggtatttca tcacgtattt tcacgacgtt ggccaatttc 240
342 aaaaatagttc tacaagaagg aaatgaaga atgtgggaag agcaaaagaa agcctctatg 300
343 ttgcaaaacc catttttgc aacgtgtcca gtgggctccc gggacagctt gtttttaaat 360
344 tcttggtctc cctgoaccgc gtccctcctt tgcctgccta gctttatgac gcatcttggg 420
345 agaacagggc agatttaaaa cctctcccca acaggcgtea aacgacatgg tgcaggctcg 480
346 ggctggggag cgggcctgcg gctgccaccg tgcataagga cttcctactc gtgcaccgcc 540
347 gcgcgctcca gggcaaaccc cagccattt agaatgtctg gaagtttctg tctctccctc 600
348 cccgtgctcg gaggccattc cccccacccc cagagcccca cctcctcctt cactgggccc 660
349 tttctaactc ctccccccta aaaccctttt caaaatgggg ttgaactggg gcggagggtt 720
350 cagtgaagccg agatgcgcc cactgactcc agcctggtga ctcctgtcca aaaaaagg 780
351 gaggggggcg ggggagagtt gaaagcttaa tatgtacttt gggggctatt aaagcaaa 840
352 ttctgactaa aggggcgaat cctcgaattg tgcgatcaag caccgagag gagagtggtg 900
353 gggggctcag aggggtgggg gctccaggga aagcccgggg gtctggcccg ggtctctc 960
354 ggggcccctc ggaaggatcg cggcccccca agtgggcggt cccgcggggc tccagctccc 1020
355 aggaagcttc gggaggctcc gcgctctggg agcccgctcg cgtggggtcc ccgcgctgca 1080
356 gcgcagaggg cccccaggg ccgcggttcc cggagcggga aagtcgccg cgggggcggt 1140
357 ggctcggggg gcgggaaggg gcggggggcg ggcgcggggc ggccagacg aatccctcc 1200
358 accgggacgc ccgcgtctg ctcgggaaga ggcggggcct gcgcgcctg cgtcgccat 1260

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/843,377

DATE: 05/14/2001

TIME: 09:23:56

Input Set : A:\RTS-0235 Sequence Listing.txt

Output Set: N:\CRF3\05142001\I843377.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date